

SeqStats version 5.1.3
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OM protein - protein search, using sw model

Run on: October 31, 2002 13:25:07 Search time 30 seconds

Query: 46-09-841-553-1
2439,921 Million emb, updated/acc

Title: US-09-841-553-1
Sequence: 1 MRFQGVALLVCLLACT.....YAYSTGNADQLKAYTTC 456

Scoring table: BLOSUM62

Gapop 10.0 Gapext 0.5

Searched: 747574 seqs, 111073756 residues

Total number of hits satisfying chosen parameters: 747574

Minimum db seq length: 0

Maximum db seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: A_Genseq_032802.*

1: /S1031/gcdatc/geneexp/geneexp-emb1/AA1980.DAT.*
2: /S1031/gcdatc/geneexp/geneexp-emb1/AA1980.DAT.*
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22: /S1031/gcdatc/geneexp/geneexp-emb1/AA1999.DAT.*

Read: 10 Is the number of results predicted by chance to have a score greater than the observed score, assuming a 1-tail and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Length	DB	ID	Description
1	3437	100.0	659	18	AM24121	Thermococcus Froese
2	2914	84.8	659	18	AM24121	MO95552; Ser ID 1
3	2914	84.8	659	18	AM24121	MO95552; Ser ID 1
4	2483.5	72.3	654	18	AM24121	Pyrococcus T. Froese
5	2118.5	62.3	554	20	AM24121	Hyperthermus a. le
6	2118.5	62.3	554	20	AM24121	Hyperthermus a. le
7	2118.5	62.3	554	20	AM24121	Hyperthermus a. le
8	1707	49.7	412	20	AM24121	Hyperthermus a. le
9	1335	27.2	188	17	AM24121	Hyperthermus a. le
10	935	27.2	188	17	AM24121	Hyperthermus a. le
11	935	27.2	188	17	AM24121	Hyperthermus a. le

12 565 15.3 731 13 AM13667
13 665 15.3 821 14 AM13668
14 665 15.3 821 14 AM13668
15 577.5 16.8 154 19 AM24127
16 577.5 16.8 154 19 AM24127
17 561.5 16.3 379 11 AM24137
18 561.5 16.3 379 11 AM24137
19 559.5 16.3 371 10 AM28742
20 559.5 16.3 371 10 AM28742
21 559.5 16.3 371 10 AM28742
22 543.5 15.8 384 15 AM45598
23 543.5 15.8 384 15 AM45598
24 543.5 15.8 384 15 AM45598
25 533.5 15.6 382 14 AM77001
26 533.5 15.6 382 14 AM77001
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36 533.5 15.6 382 14 AM77001
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45 533.5 15.6 382 14 AM77001

ALIGNMENTS

RESULT 1
AM24121
10 AM24121 standard: Protein; 659 AA.
AC AM24121.
XX 20-APR-1998 (first entry;
DE Thermococcus Froese.
XX Process; research reagent; thermal stability, thermococcus color.
XX Thermococcus color DSM-1171.
PN MO971423-AL.
XX MO95552; Ser ID 1.
XX MO95552; Ser ID 1.
PP 07-NOV-1995; 96AC-JP01-12
PR 12-DEC-1995; 95JP-032 (10)
XX (TAKA) TAKANA SHUJO CO LTD.
XX Asada K, Kato I, Mitte K,
XX Tsunashima S, Yamamoto K,
XX Morioka M, Takahara H;
XX WPI: 1997-31279/30.
XX N-PS08: AM25567.
XX Process(es) and genes encoding them obtained from thermococcus and
XX Pyrococcus strains - have extremely high thermal stability and are
XX useful industrially and as research reagents

[illegible]

QY 443 P---TSCNKGKSNH-----FDUSCATPTATLWOTGSSDOLLYDPN 490
 DB : : : : :
 QY 486 TRNLOEDYTLISATGKGAKAPGFTLGAJLTPA---NGTANVOTRUSJG 502
 DB : : : : :
 QY 491 EUCSTATYCFKVGTYNPTAGTNYKHYR-----KGANW 529
 DB : : : : :
 QY 553 AUGOTTSATYATGAGSYETAANVREVESTNYLKLDRSCATYANTALSGUTEL 612
 DB : : : : :
 QY 530 -----VWVSQSL--OSG-----GNPNPNPPTG 558
 DB : : : : :
 QY 613 KQSTAPYADGNGOTRYFGDSTVJASVLGADPTFRICAKLACPLDYNTYTD 572
 DB : : : : :
 QY 560 TO-----TFGSDYNOTDFTFMNYSKATIGDLEFDSNCLDYLDPGHL 612
 DB : : : : :
 QY 673 ARKAPKYVYFGAKAKAFADYLTENBSAVTGNLENYSFESAIL-----GQ 725
 DB : : : : :
 QY 727 INGTLSQON-MYHESKAKOYT 749

Search completed: October 31, 2002, 13:25:40
 Job time : 34 secs

1 APPLICANT: TAKAKURA, HIRAKU
 2 CLASSING DATE: 20-MAY-1998
 3 PRIOR APPLICATION DATA:
 4 PRIORITY NUMBER: PCT/JP95/02183
 5 PUBLICATION NUMBER: 136
 6 PRIOR APPLICATION DATA: 136
 7 APPLICATION NUMBER: JP 32385/1995
 8 ATORNEY/AGENT INFORMATION:
 9 BUDSON, Stacey L.
 10 BUDSON, Stacey L.
 11 REFERENCE/DOCKET NUMBER: TAKAKURA-1
 12 TELECOMMUNICATION INFORMATION:
 13 TELEPHONE: (202) 737-5527
 14 TELEFAX: (202) 737-5528
 15 INFORMATION FOR SEQ ID NO: 3:
 16 LENGTH: 522 amino acids
 17 TYPE: amino acid
 18 TOPOLOGY: linear
 19 MOLECULE TYPE: peptide
 20 OTHER INFORMATION: /note= xaa at position 428 is Gly or Val.

US-08-894-518B-3

Query Match 62.2% Score 313.5 DD 4; Length 522;
 Best Local Similarity 78.3% Pred no gaps 70; Indels 7; Gaps 3;
 Matches 407; Conservative 36; Miscellaneous 70;
 Qy 141 VSGDQAVTWNISLGDQGVVVALDTGIDANHPLEKRYGVYVNGVSGSTPTDGH 200
 Db 9 SAQYMTTWN-LGTDGSSITGIDTIDGIDASHPDQKRYGVYVNGVSGSTPTDGH 67
 Qy 201 GTHTACVAGTGV-NHQITGVAPKALGVKYGADGDSVSTIACQVYVNDKYG 259
 Db 68 GTHTASGTGASGKRGKAPFLKGLTIIIIIIIIIIIIIIIIIIIIIIIIIIIIII 127
 Qy 260 IRYVNLGSGDSGDSGDSGDSGDSGDSGDSGDSGDSGDSGDSGDSGDSGDSG 259
 Db 128 IRYVNLGSGDSGDSGDSGDSGDSGDSGDSGDSGDSGDSGDSGDSGDSGDS 127
 Qy 320 GAVSNQNTASTFSRQFPGHLPYVGVGVDTAPRAGSGSTPTDPTVASTEN 379
 Db 188 GAVDITDITFSRQFPGHLPYVGVGVDTAPRAGSGSTPTDPTVASTEN 379
 Qy 380 APTHSVGVGLLQNHPTVQVYKALITADYAPKADYAPKADYAPKADYAPKADY 439
 Db 248 APTHAGVGLLQNHPTVQVYKALITADYAPKADYAPKADYAPKADYAPKADY 439
 Qy 440 YALPFGSGDGNFTDTSATPTTATMOTSSBILTYDPKNGVSTAY 499
 Db 308 YALPFGSGDGNFTDTSATPTTATMOTSSBILTYDPKNGVSTAY 499
 Qy 500 YKGVACVYTPACVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVY 559
 Db 308 YKGVACVYTPACVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVY 559
 Qy 560 TQFTFVGVNDVSDPTFVGVNDVSDPTFVGVNDVSDPTFVGVNDVSDPTFV 622
 Db 358 YKGVACVYTPACVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVY 622
 Qy 620 NSTEVTAMHPQNTPLVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYV 682
 Db 420 NSTEVTAMHPQNTPLVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYV 682
 Qy 483 NSTEVTAMHPQNTPLVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYV 522
 Db 483 NSTEVTAMHPQNTPLVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYV 522

RESULT 7
 US-09-445-472-4
 1 PRESUMED 1. Application US/09/445/472
 2 GENERAL INFORMATION:
 3 APPLICANT: TAKAKURA, HIRAKU
 4 APPLICANT: TAKAKURA, HIRAKU
 5 APPLICANT: SHIMOD, TORUO
 6 APPLICANT: ASHIDA, KIYOZO

1 APPLICANT: TAKAKURA, HIRAKU
 2 APPLICANT: SHIMODA, TORUO
 3 APPLICANT: ASHIDA, KIYOZO
 4 TITLE: TAKAKURA, HIRAKU
 5 TITLE: TAKAKURA, HIRAKU
 6 TITLE: TAKAKURA, HIRAKU
 7 TITLE: TAKAKURA, HIRAKU
 8 TITLE: TAKAKURA, HIRAKU
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 97 TITLE: TAKAKURA, HIRAKU
 98 TITLE: TAKAKURA, HIRAKU
 99 TITLE: TAKAKURA, HIRAKU
 100 TITLE: TAKAKURA, HIRAKU

RESULT 8
 US-09-445-472-1
 1 PRESUMED 1. Application US/09/445/472
 2 GENERAL INFORMATION:
 3 APPLICANT: TAKAKURA, HIRAKU
 4 APPLICANT: TAKAKURA, HIRAKU
 5 APPLICANT: SHIMODA, TORUO
 6 APPLICANT: ASHIDA, KIYOZO

ATTORNEY/AGENT INFORMATION:
 REGISTRATION NUMBER: 5665
 REFERENCE/DOCKET NUMBER: 5051-260
 TELEPHONE: (913) 881-3175
 INVESTIGATOR: (913) 881-3175
 SEQUENCE CHARACTERIZATION NO: 2
 LENGTH: 379 amino acids
 MOLECULE TYPE: protein
 TOPOLOGY: single chain
 ORIGIN: natural
 ORGANISM: Bacillus licheniformis
 US-08-483-774-2 Ptd-1

Query Match Similarity: 16.3% Score 560.5; DB 1: Length 379;
 Matches 150; Conservative: 53; Mismatches 133; Indels 49; Gaps 34;

Qy 57 MDVDTTMMGTGDRDAY-VLRMGQVATSKLIPAVKTKADLLAGHIDT 114
 Db 35 WEDVDTTMMGTGDRDAY-VLRMGQVATSKLIPAVKTKADLLAGHIDT 63
 Qy 115 GFYGVRSVSKTLDYVDVDDT---SVSGIDGDPNNKSGTGGSVVALVDGID 171
 Db 94 AT-----VEEDVPMALQVYTGTFPLTAA-----SVSGIDGDPNNKSGTGGSVVALVDGID 171
 Qy 172 ANHPDQKGVKGVNDVNGSTPDQDQGVNAGVAGTGVNSGVSDVAPKALVDK 331
 Db 142 ASHPDL---NVYGGASTVAGKATVNDQNGSTVATVVALDNTG-VLGVAFSVLAK 158
 Qy 232 VLQAGSGSVSTIAGGVYVQHKQGVIRVNLGSGSGDGLSGLQVNAKNGVI 261
 Db 158 VLQSGSGSVSTIAGGVYVQHKQGVIRVNLGSGSGDGLSGLQVNAKNGVI 261
 Qy 293 VYVAMGSGSVSTIAGGVYVQHKQGVIRVNLGSGSGDGLSGLQVNAKNGVI 291
 Db 293 VYVAMGSGSVSTIAGGVYVQHKQGVIRVNLGSGSGDGLSGLQVNAKNGVI 291
 Qy 350 QVDTAPRSLGSGTGTGTPADVSVIAGVNSKASSTSVG-----ALETMAP 305
 Db 350 QVDTAPRSLGSGTGTGTPADVSVIAGVNSKASSTSVG-----ALETMAP 305
 Qy 306 G-----AGVYTTPTTAT-LQNTSNVPMAGMALLKLNPNASQVNNKLS 358
 Db 306 G-----AGVYTTPTTAT-LQNTSNVPMAGMALLKLNPNASQVNNKLS 358
 Qy 357 TATLIG-----SFTDTGLGLNIPAA 377
 Db 357 TATLIG-----SFTDTGLGLNIPAA 377

RESULT 14
 US-07-923-260A-4
 Patent No. 5102022
 GENERAL INFORMATION:

TITLE OF INVENTION: Mesozyme
 TITLE OF INVENTION: Mesozyme
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS: Mesozyme
 STREET: 230 South Fifteenth Street, Suite 500
 CITY: Philadelphia
 STATE: PA
 COUNTRY: USA
 ZIP: 19102

COMPUTER: IBM PC compatible
 MEDIUM TYPE: floppy disk
 SOFTWARE: Patent In 2000/AM-005
 CURRENT APPLICATION DATA: Version 11.25

APPLICATION NUMBER: US-07-923-260A
 REGISTRATION NUMBER: 5665
 REFERENCE/DOCKET NUMBER: 5051-260
 TELEPHONE: (913) 881-3175
 INVESTIGATOR: (913) 881-3175
 SEQUENCE CHARACTERIZATION NO: 2
 LENGTH: 379 amino acids
 MOLECULE TYPE: protein
 TOPOLOGY: single chain
 ORIGIN: natural
 ORGANISM: Bacillus licheniformis
 US-08-483-774-2 Ptd-1

Query Match Similarity: 16.3% Score 557.5; DB 1: Length 350;
 Matches 146; Conservative: 56; Mismatches 134; Indels 49; Gaps 13;

Qy 57 MDVDTTMMGTGDRDAY-VLRMGQVATSKLIPAVKTKADLLAGHIDT 114
 Db 6 NYKDTTMMGTGDRDAY-VLRMGQVATSKLIPAVKTKADLLAGHIDT 114
 Qy 115 GFYGVRSVSKTLDYVDVDDT---SVSGIDGDPNNKSGTGGSVVALVDGID 171
 Db 55 AT-----VEEDVPMALQVYTGTFPLTAA-----SVSGIDGDPNNKSGTGGSVVALVDGID 171
 Qy 172 ANHPDQKGVKGVNDVNGSTPDQDQGVNAGVAGTGVNSGVSDVAPKALVDK 331
 Db 113 ASHPDL---NVYGGASTVAGKATVNDQNGSTVATVVALDNTG-VLGVAFSVLAK 331
 Qy 232 VLQAGSGSVSTIAGGVYVQHKQGVIRVNLGSGSGDGLSGLQVNAKNGVI 391
 Db 170 VLQSGSGSVSTIAGGVYVQHKQGVIRVNLGSGSGDGLSGLQVNAKNGVI 391
 Qy 293 VYVAMGSGSVSTIAGGVYVQHKQGVIRVNLGSGSGDGLSGLQVNAKNGVI 391
 Db 293 VYVAMGSGSVSTIAGGVYVQHKQGVIRVNLGSGSGDGLSGLQVNAKNGVI 391
 Qy 350 QVDTAPRSLGSGTGTGTPADVSVIAGVNSKASSTSVG-----ALETMAP 409
 Db 277 QVDTAPRSLGSGTGTGTPADVSVIAGVNSKASSTSVG-----ALETMAP 409
 Qy 410 TADVAPRSLGSGTGTGTPADVSVIAGVNSKASSTSVG-----ALETMAP 434
 Db 338 TATLIG-----SFTDTGLGLNIPAA 348

RESULT 15
 US-08-845-295A-1
 Sequence 1: Application US/08/45255A
 GENERAL INFORMATION:

TITLE OF INVENTION: Enzymatic Process for the Manufacture of
 TITLE OF INVENTION: Enzymatic Process for the Manufacture of
 NUMBER OF SEQUENCES: 3
 CORRESPONDENCE ADDRESS: Mesozyme
 STREET: 230 South Fifteenth Street, Suite 500
 CITY: Philadelphia
 STATE: PA
 COUNTRY: USA
 ZIP: 19102

COMPUTER: IBM PC compatible
 MEDIUM TYPE: floppy disk
 SOFTWARE: Patent In 2000/AM-005
 CURRENT APPLICATION DATA: Version 11.25

[illegible]

Search completed: October 31, 2002, 13:32:26
Job time : 17 secs

Db 206 YSTYPTPTAT-1AGTNSATVGVAGAAIIISHPLASGVNR-LESTATIG-...-SS 743

Qy 422 IAGVGAGVYVYA 434

Db 251 FTGTGTGTLTMDFA 273

RESULT 10

C-Function: EC 3.1.21.1 precursor - Thermotactonomeyes sp. (strain 179)
C-Species: Thermotactonomeyes sp.

C-Accession: J04802

C-Revision: 1995 sequence revision 15-Oct-1995 text_change 09-Jun-2002

C-Comment: J04802

C-Reference: J04802

C-Title: Purification and characterization of a thermostable alkaline protease from *Thermotactonomeyes* sp.

C-Reference number: J04802; M020:9551070

C-Molecule type: DNA

C-Accession: J04802

C-Revision: 1995 sequence revision 15-Oct-1995 text_change 09-Jun-2002

C-Comment: This protein is thermostable.

C-Function: on extracellular alkaline serine protease (validated, M020:95241370)

C-Superfamily: subtilisin, subtilisin homology

C-Cleavage: hydrolysis; serine protease

C-F107-387/Product: alkaline protease status experimental <M07>

C-F107-387/Product: alkaline protease status experimental <M07>

C-F107-387/Product: alkaline protease status experimental <M07>

C-F107-387/Product: alkaline protease status experimental <M07>

C-F107-387/Product: alkaline protease status experimental <M07>

C-F107-387/Product: alkaline protease status experimental <M07>

C-F107-387/Product: alkaline protease status experimental <M07>

C-F107-387/Product: alkaline protease status experimental <M07>

C-F107-387/Product: alkaline protease status experimental <M07>

C-F107-387/Product: alkaline protease status experimental <M07>

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C-F107-387/Product: alkaline protease status experimental <M07>

C-F107-387/Product: alkaline protease status experimental <M07>

C-F107-387/Product: alkaline protease status experimental <M07>

subtilisin (EC 3.1.21.62; MAT 3900000 - Bacillus subtilis (accession NC2-1)

C-Species: Bacillus subtilis

C-Accession: J04802

C-Revision: 1995 sequence revision 15-Oct-1995 text_change 21-Jul-2000

C-Comment: J04802

C-Reference: J04802

C-Title: Purification and characterization of a thermostable alkaline protease from *Thermotactonomeyes* sp.

C-Reference number: J04802; M020:9551070

C-Molecule type: DNA

C-Accession: J04802

C-Revision: 1995 sequence revision 15-Oct-1995 text_change 21-Jul-2000

C-Comment: J04802

C-Function: on extracellular alkaline serine protease (validated, M020:95241370)

C-Superfamily: subtilisin, subtilisin homology

C-Cleavage: hydrolysis; serine protease

C-F107-387/Product: alkaline protease status experimental <M07>

C-F107-387/Product: alkaline protease status experimental <M07>

C-F107-387/Product: alkaline protease status experimental <M07>

C-F107-387/Product: alkaline protease status experimental <M07>

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Wed Nov 6 14:29:31 2002

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Page 10

Search completed: October 31, 2002, 13:31:55
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Wed Nov 6 14:29:32 2002

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 Db 94 AT-----VEEDNVAHLYGTVPGLKADY-QQGFQGANVYVLDLQ 341
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 Db 357 TATYLG---SFSFGRLINVEAA 377

Search completed: October 31, 2002, 13:31:14
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GenCode version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 2, 2002, 05:31:18 Search time 3395.5 seconds
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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues 4109280

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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VERSION: US-09-841-553-2
SOURCE: US-09-841-553-2
ORGANISM: US-09-841-553-2

Unclassified
Reference
Takura, H., Morita, M., Shimoto, T., Asada, K. and Noto, I.
Thermotable protease
Patent: US 6,358,726
Date: 18 MAR 2002
Qualifiers

Prod. No. is the number of results predicted by chance to have a

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BASE COUNT
ORIGIN


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Db 20955 CTTCCGACAGTTTGCA-----CGGCACTCGCGGTACGACGGTTCCAGCGGGGAG_20903
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Db 20902 CGCGCGGATGAGAGTGGACCGCGCGCGGGGTGGCGCGGGGTGATGCGCTCGCGACCGCTA_20813
Oy 1338 CGGCTCTGTCGCGGACAGGAGGCGGACACACACCTTCGACGTCAGCGGCGCGACCTT_1397
Db 20812 CCGCGCGGCGGAGCTCGCGGCGCGCGCGCGCTTGGTACGTCACGACGACGCG_20783
Oy 1398 CGTAGCGGACCTT_1412
Db 20782 CGCGGCGGTCACTT_20768

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Search completed: November 2, 2002, 10:23:32
 Job time : 3523.5 sec

QY 1304 TQAGTACGAGCTACGACGAGCTACGCTACGCTGCGGAGAGGAGG 1363
 Db 1304 TQAGTACGAGCTACGAGCTACGCTACGCTGCGGAGAGGAGG 1363
 QY 1364 CAGCCAGAGCTACGCTACGAGGAGGAGGAGGAGGAGGAGGAGG 1423
 Db 1364 CAGCCAGAGCTACGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1423
 QY 1424 CAGGAGCTACGAGCTACGAGCTACGAGCTACGAGCTACGAGCT 1483
 Db 1424 CAGGAGCTACGAGCTACGAGCTACGAGCTACGAGCTACGAGCT 1483
 QY 1484 CAGGAGCTACGAGCTACGAGCTACGAGCTACGAGCTACGAGCT 1543
 Db 1484 CAGGAGCTACGAGCTACGAGCTACGAGCTACGAGCTACGAGCT 1543
 QY 1544 CAGGAGCTACGAGCTACGAGCTACGAGCTACGAGCTACGAGCT 1603
 Db 1544 CAGGAGCTACGAGCTACGAGCTACGAGCTACGAGCTACGAGCT 1603
 QY 1604 CAGGAGCTACGAGCTACGAGCTACGAGCTACGAGCTACGAGCT 1663
 Db 1604 CAGGAGCTACGAGCTACGAGCTACGAGCTACGAGCTACGAGCT 1663
 QY 1664 CAGGAGCTACGAGCTACGAGCTACGAGCTACGAGCTACGAGCT 1723
 Db 1664 CAGGAGCTACGAGCTACGAGCTACGAGCTACGAGCTACGAGCT 1723
 QY 1724 CAGGAGCTACGAGCTACGAGCTACGAGCTACGAGCTACGAGCT 1783
 Db 1724 CAGGAGCTACGAGCTACGAGCTACGAGCTACGAGCTACGAGCT 1783
 QY 1784 CAGGAGCTACGAGCTACGAGCTACGAGCTACGAGCTACGAGCT 1843
 Db 1784 CAGGAGCTACGAGCTACGAGCTACGAGCTACGAGCTACGAGCT 1843
 QY 1844 CAGGAGCTACGAGCTACGAGCTACGAGCTACGAGCTACGAGCT 1903
 Db 1844 CAGGAGCTACGAGCTACGAGCTACGAGCTACGAGCTACGAGCT 1903
 QY 1904 CAGGAGCTACGAGCTACGAGCTACGAGCTACGAGCTACGAGCT 1963
 Db 1904 CAGGAGCTACGAGCTACGAGCTACGAGCTACGAGCTACGAGCT 1963
 QY 1964 CAGGAGCTACGAGCTACGAGCTACGAGCTACGAGCTACGAGCT 2023
 Db 1964 CAGGAGCTACGAGCTACGAGCTACGAGCTACGAGCTACGAGCT 2023

RESULT 4
 US-08-894-818B-15
 REQUESTED BY: 4261822
 GENERAL INFORMATION

APPLICANT: TAKAHARA, HILARU
 APPLICANT: YAMAKOTO, Katsuhiko
 APPLICANT: MITTA, Masaoori
 APPLICANT: TSUNAKAWA, Susumu
 APPLICANT: KATO, Kunoshin
 TITLE OF INVENTION: HYPERTEXTHOSTABLE PROTEASE GENES
 ADDRESS: 4261822
 CORRESPONDENCE ADDRESS: 4261822

US-08-894-818B-15
 STATE: D.C.
 CITY: Washington
 COUNTRY: United States of America
 COMPUTER: 201004
 COMPUTER REABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT RELEASE: 11.0
 APPLICATION NUMBER: US/08/894,818B
 FILING DATE: 20-MAY-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 577/P96/03253
 APPLICATION DATE: 20-MAY-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP-323285/1995
 APPLICATION DATE: 20-MAY-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Brody, Roger L.
 REGISTRATION NUMBER: 25,618
 TELECOMMUNICATION INFORMATION:
 INFORMATION FOR SEQ ID NO. 15:
 SOURCE CHARACTERISTICS:
 LENGTH: 155 base pair-s
 TYPE: unknown
 STRANDNESS: double
 TOPOLOGY: linear
 MOLECULE: genomic DNA

US-08-894-818B-15

Query Match
 Best Match: 100.0%, 28/28, 234
 Matches: 1165; Conservative 0; Mismatches 0; Gaps 0;

QY 813 GAGCTCGAGCAACGACCTCCCTCAGTCAAGGCGCTCAACAGCGCTGGACCGCGTAT 872
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 QY 873 AGTAGTCTGCTGCGCGCGCGACAGCGCGCGACAGCTACAGCTCGGCTCACCGC 932
 Db 61 AGTAGTCTGCTGCGCGCGCGACAGCGCGCGACAGCTACAGCTCGGCTCACCGC 932
 QY 933 CGCGCGGAGAGCTCATACGCTCGCTCAAGTTCAGAGAGAGCAACATCGACGCTT 992
 Db 61 AGTAGTCTGCTGCGCGCGCGACAGCGCGCGACAGCTACAGCTCGGCTCACCGC 120
 Db 121 CGCGCGGAGAGCTCATACGCTCGCTCAAGTTCAGAGAGAGCAACATCGACGCTT 180
 QY 993 CTCACAGGAGAGCTCGCGCGCGCGACAGCTACAGCGAGAGTTCGCTCGCGCGCT 1052
 Db 181 CTCACAGGAGAGCTCGCGCGCGCGACAGCTACAGCGAGAGTTCGCTCGCGCGCT 240
 QY 1053 TGAAGTTCAGTCAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTA 1112
 Db 241 TGAAGTTCAGTCAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTA 1112
 QY 1113 CACACAGGCTCTGAGTACAGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTA 1172
 Db 301 CACACAGGCTCTGAGTACAGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTA 1172
 Db 301 CACACAGGCTCTGAGTACAGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTA 1172
 QY 1173 CTCACAGGCTCTGAGTACAGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTA 1232
 Db 361 CTCACAGGCTCTGAGTACAGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTA 1232
 QY 1233 CAGATAGTTCGCTA 1292
 Db 481 CAGATAGTTCGCTA 1292
 QY 1293 CAGATAGTTCGCTA 1352
 Db 540 CAGATAGTTCGCTA 1352
 QY 1353 CAGATAGTTCGCTA 1412
 Db 600 CAGATAGTTCGCTA 1412
 QY 1413 CAGATAGTTCGCTA 1472

QY 1336 CATAGTCGCGCCGAGGATAGCGAGTACGCTGCGGTGCGGTGAGGTGAGTCTA 2295
 DB 840 TATCTATACGCGAGGATAGCGAGTACGCTGCGGTGAGGTGAGTCTA 899
 QY 1396 GAGGCGCTGAGTACGCGAGTACGCGAGTACGCTGCGGTGAGGTGAGTCTA 1355
 DB 900 GAGGCGCTGAGTACGCGAGTACGCGAGTACGCTGCGGTGAGGTGAGTCTA 950
 QY 1356 GCGAGCGCGAGTACGCGAGTACGCGAGTACGCTGCGGTGAGGTGAGTCTA 1415
 DB 960 GCGAGCGCGAGTACGCGAGTACGCGAGTACGCTGCGGTGAGGTGAGTCTA 1019
 QY 1416 GCGAGCGCGAGTACGCGAGTACGCGAGTACGCTGCGGTGAGGTGAGTCTA 1475
 DB 1020 GCGAGCGCGAGTACGCGAGTACGCGAGTACGCTGCGGTGAGGTGAGTCTA 1079
 QY 1476 GAGTACGCTGAGTACGCGAGTACGCGAGTACGCTGCGGTGAGGTGAGTCTA 1535
 DB 1080 GAGTACGCTGAGTACGCGAGTACGCGAGTACGCTGCGGTGAGGTGAGTCTA 1139
 QY 1536 GCGAGCGCGAGTACGCGAGTACGCGAGTACGCTGCGGTGAGGTGAGTCTA 1595
 DB 1140 GCGAGCGCGAGTACGCGAGTACGCGAGTACGCTGCGGTGAGGTGAGTCTA 1199
 QY 1596 GCGAGCGCGAGTACGCGAGTACGCGAGTACGCTGCGGTGAGGTGAGTCTA 1655
 DB 1200 GCGAGCGCGAGTACGCGAGTACGCGAGTACGCTGCGGTGAGGTGAGTCTA 1244
 QY 1656 GCGAGCGCGAGTACGCGAGTACGCGAGTACGCTGCGGTGAGGTGAGTCTA 1715
 DB 1245 GCGAGCGCGAGTACGCGAGTACGCGAGTACGCTGCGGTGAGGTGAGTCTA 1304
 QY 1716 GCGAGCGCGAGTACGCGAGTACGCGAGTACGCTGCGGTGAGGTGAGTCTA 1775
 DB 1305 GCGAGCGCGAGTACGCGAGTACGCGAGTACGCTGCGGTGAGGTGAGTCTA 1364
 QY 1776 GAGTACGCTGAGTACGCGAGTACGCGAGTACGCTGCGGTGAGGTGAGTCTA 1835
 DB 1365 GAGTACGCTGAGTACGCGAGTACGCGAGTACGCTGCGGTGAGGTGAGTCTA 1444
 QY 1836 GCGAGCGCGAGTACGCGAGTACGCGAGTACGCTGCGGTGAGGTGAGTCTA 1895
 DB 1425 GCGAGCGCGAGTACGCGAGTACGCGAGTACGCTGCGGTGAGGTGAGTCTA 1484
 QY 1896 GCGAGCGCGAGTACGCGAGTACGCGAGTACGCTGCGGTGAGGTGAGTCTA 1955
 DB 1485 GCGAGCGCGAGTACGCGAGTACGCGAGTACGCTGCGGTGAGGTGAGTCTA 1544
 QY 1956 GCGAGCGCGAGTACGCGAGTACGCGAGTACGCTGCGGTGAGGTGAGTCTA 2015
 DB 1545 GCGAGCGCGAGTACGCGAGTACGCGAGTACGCTGCGGTGAGGTGAGTCTA 1565

RESULT 10

US-09-445-472-2

Patent No. 6,359,728

GENERAL INFORMATION:

APPLICANT: NIKENU

APPLICANT: MORISHITA, MIO

APPLICANT: SHIMIZU, Tomoko

APPLICANT: ASANO, Kiyoko

APPLICANT: KAWANO, Shin

TITLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE

FILE REFERENCE: TAKAHARA-6 US/09/445, 472

CURRENT FILING DATE: 1999-12-06

PRIORITY FILING DATE: 1999-12-06

PRIORITY FILING DATE: 1999-12-06

PRIORITY FILING DATE: 1999-12-06

PRIORITY FILING DATE: 1999-12-06

PRIORITY FILING DATE: 1999-12-06

PRIORITY FILING DATE: 1999-12-06

PRIORITY FILING DATE: 1999-12-06

PRIORITY FILING DATE: 1999-12-06

PRIORITY FILING DATE: 1999-12-06

PRIORITY FILING DATE: 1999-12-06

PRIORITY FILING DATE: 1999-12-06

TYPE: DNA
 ORGANISM: Artificial Sequence
 OTHER INFORMATION: Synthetic
 US-09-445-472-2

Query Match

Best Local Similarity

Matches 796

28.3% Score 560.4; DB 4; Length 1236;

No. 1.4e-103; Identities 3; Gaps 1;

QY 459 CTGCGCTGACGCGAGCGCTGCGGTGCGGTGAGGTGAGTCTA 318

DB 60 GTTGGATATGCGGTGCGGTGCGGTGAGGTGAGTCTA 119

QY 510 CATCGCTGCGCGAGCGCTGCGGTGCGGTGAGGTGAGTCTA 378

DB 120 CATCGCTGCGCGAGCGCTGCGGTGCGGTGAGGTGAGTCTA 179

QY 578 GCGAGCGCGAGTACGCGAGTACGCGAGTACGCTGCGGTGAGGTGAGTCTA 438

DB 180 TCGATGCGCGAGTACGCGAGTACGCGAGTACGCTGCGGTGAGGTGAGTCTA 339

QY 639 CG-----TTAATCGCGAGTACGCGAGTACGCGAGTACGCTGCGGTGAGGTGAGTCTA 495

DB 240 AGCATGATGCGCGAGTACGCGAGTACGCGAGTACGCTGCGGTGAGGTGAGTCTA 299

QY 696 TCTGCGCTGCGCGAGTACGCGAGTACGCGAGTACGCTGCGGTGAGGTGAGTCTA 755

DB 300 TCTGCGCTGCGCGAGTACGCGAGTACGCGAGTACGCTGCGGTGAGGTGAGTCTA 359

QY 756 CGAGCGAGTACGCGAGTACGCGAGTACGCTGCGGTGAGGTGAGTCTA 815

DB 360 TCGATGCGCGAGTACGCGAGTACGCGAGTACGCTGCGGTGAGGTGAGTCTA 419

QY 816 CTGCGCGAGTACGCGAGTACGCGAGTACGCTGCGGTGAGGTGAGTCTA 875

DB 420 CTGCGCGAGTACGCGAGTACGCGAGTACGCTGCGGTGAGGTGAGTCTA 479

QY 876 AGTCTGCGCGAGTACGCGAGTACGCGAGTACGCTGCGGTGAGGTGAGTCTA 935

DB 480 AGTCTGCGCGAGTACGCGAGTACGCGAGTACGCTGCGGTGAGGTGAGTCTA 539

QY 936 GCGAGCGCGAGTACGCGAGTACGCGAGTACGCTGCGGTGAGGTGAGTCTA 995

DB 540 GCGAGCGCGAGTACGCGAGTACGCGAGTACGCTGCGGTGAGGTGAGTCTA 599

QY 996 GCGAGCGCGAGTACGCGAGTACGCGAGTACGCTGCGGTGAGGTGAGTCTA 1055

DB 600 GCGAGCGCGAGTACGCGAGTACGCGAGTACGCTGCGGTGAGGTGAGTCTA 659

QY 1056 CATCATGCGCGAGTACGCGAGTACGCGAGTACGCTGCGGTGAGGTGAGTCTA 1115

DB 660 CATCATGCGCGAGTACGCGAGTACGCGAGTACGCTGCGGTGAGGTGAGTCTA 719

QY 1116 GAGGCGCTGAGTACGCGAGTACGCGAGTACGCTGCGGTGAGGTGAGTCTA 1175

DB 720 GAGGCGCTGAGTACGCGAGTACGCGAGTACGCTGCGGTGAGGTGAGTCTA 779

QY 1176 GAGGCGCTGAGTACGCGAGTACGCGAGTACGCTGCGGTGAGGTGAGTCTA 1235

DB 780 GAGGCGCTGAGTACGCGAGTACGCGAGTACGCTGCGGTGAGGTGAGTCTA 835

QY 1236 CATGAGTCTGCGCGAGTACGCGAGTACGCGAGTACGCTGCGGTGAGGTGAGTCTA 1295

DB 840 CATGAGTCTGCGCGAGTACGCGAGTACGCGAGTACGCTGCGGTGAGGTGAGTCTA 899

QY 1296 GAGGCGCTGAGTACGCGAGTACGCGAGTACGCTGCGGTGAGGTGAGTCTA 1355

DB 900 GAGGCGCTGAGTACGCGAGTACGCGAGTACGCTGCGGTGAGGTGAGTCTA 959

QY 1356 GCGAGCGCGAGTACGCGAGTACGCGAGTACGCTGCGGTGAGGTGAGTCTA 1415

DB 960 GCGAGCGCGAGTACGCGAGTACGCGAGTACGCTGCGGTGAGGTGAGTCTA 1019


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1 CURRENT APPLICATION DATA:
2 PCT NO. 98/08/894, 8188
3 FILING DATE 20-MAY-1998
4 CLASSIFICATION: 435
5 PRIOR APPLICATION DATA:
6 PCT/JP98/01233
7 FILING DATE 07-NOV-1996
8 PRIOR APPLICATION DATA: JP 332385/1995
9 FILING DATE 12-DEC-1995
10 PCT/JP98/01233
11 FILING DATE 07-NOV-1996
12 ATTORNEY/AGENT INFORMATION:
13 NAME: KAWASAKI, KENJI
14 REGISTRATION NUMBER: 25 618
15 REFERENCE/DOCKET NUMBER: TAKAURA-1
16 TELECOMMUNICATIONS INFORMATION:
17 TELEPHONE: (03) 737-3228
18 TELEFAX: (03) 737-3228
19 INFORMATION FOR SEQ ID NOS: 14:
20 SOURCE: 364 base pairs
21 LENGTH: 364 base pairs
22 TYPE: nucleic acid
23 STRANES: single
24 TOPOLOGY: linear
25 MOLECULE TYPE: other nucleic acid
26
27 US-08-894-8188-14
28
29 Query Match 26.94: score 512.8; DB 4: Length 364:
30 Best Local Similarity 97.04: pred. No 3,94-98:
31 Matches 340; Conservative 0; Mismatches 17; Indels 0; Gaps 0.
32
33 Oy 598 CAGGACGACGCTTCCGGGTATGCTTCCGGACGCGACGCTTACTCTCCGTAATA 657
34 Db 4 CAGGACGACGCTTCCGGGTATGCTTCCGGACGCGACGCTTACTCTCCGTAATA 63
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36 Oy 658 GCGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 717
37 Db 64 GCGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
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39 Oy 718 AGCGTTCGACATATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 777
40 Db 124 AGCGTTCGACATATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 783
41
42 Oy 778 ATGCGTTCGACATATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 837
43 Db 184 ATGCGTTCGACATATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 843
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45 Oy 838 ATGCGTTCGACATATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 897
46 Db 244 ATGCGTTCGACATATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 903
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48 Oy 898 AGCGTTCGACATATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 957
49 Db 304 AGCGTTCGACATATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 310
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51 Oy 958 GTCGCGTTCGACATATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1017
52 Db 424 GTCGCGTTCGACATATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 430
53
54 Oy 1018 CGAGCGTTCGACATATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1077
55 Db 424 CGAGCGTTCGACATATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 430
56
57 Oy 1078 AGCGTTCGACATATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1137
58 Db 484 AGCGTTCGACATATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 490
59
60 Oy 1138 GCGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1197
61 Db 544 GCGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 550
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63 RESULT 13
64 US 97-080-016-1

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1 Sequence 1, Application US/09000016
2 Patent No. 614541
3 Applicant: ALICIA ALIWA ET AL.
4 TITLE OF INVENTION: GENE ENCODING A PROTEIN HAVING ASYMMETRIC
5 C-TERMINUS AND A 4-SUBSTITUTED 1,4-DIHYDROXYPIRIMIDINE DE
6 RIVATION PRODUCT
7 NUMBER OF SEQUENCES: 7
8 ADDRESS: 2033 K Street, N.W. #800
9 CITY: Washington
10 STATE: D.C.
11 COUNTRY: U.S.A.
12 ZIP: 20006
13 MEDIAN TYPE: Diskette, 3.5 inch, 1.44 mb
14 COMPUTER: IBM Compatible
15 SOFTWARE: MicroPerfect 3.1
16 CURRENT APPLICATION DATA:
17 PUBLICATION NUMBER: 03/09/0030, 016
18 FILING DATE: 07/07/98
19 CLASSIFICATION: 530
20 PRIOR APPLICATION DATA:
21 REFERENCE/DOCKET NUMBER:
22 FILING DATE:
23 ATTORNEY/AGENT INFORMATION:
24 NAME: KAWASAKI, KENJI
25 REGISTRATION NUMBER: 25 618
26 REFERENCE/DOCKET NUMBER: TAKAURA-1
27 TELECOMMUNICATIONS INFORMATION:
28 TELEPHONE: (03) 737-3228
29 TELEFAX: (03) 737-3228
30 INFORMATION FOR SEQ ID NO. 1:
31 SOURCE: 2809 base pairs
32 LENGTH: 2809 base pairs
33 STRANES: single
34 TOPOLOGY: linear
35 MOLECULE TYPE: genomic DNA
36 STRANES: single
37 ORGANISM: Streptococcus viridansporus
38 STRAIN: A-514
39 ORGANISM: Streptococcus viridansporus
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41 STRAIN: A-514
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95 STRAIN: A-514
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97 STRAIN: A-514
98 ORGANISM: Streptococcus viridansporus
99 STRAIN: A-514
100 ORGANISM: Streptococcus viridansporus

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Query Match 26.94: score 101.6; DB 3: Length 2809;

Best Local Similarity 51.94: Pred. No 7, 1e-30;

Matches 593; Conservative 0; Mismatches 439; Indels 48; Gaps 8;

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1 Oy 312 TGTATGACGCGGTACTGCTGCTATACACAGCGCTCTCGCGGTAAAGCTCATACAGGAG 391
2 Db 870 TGTATGACGCGGTACTGCTGCTATACACAGCGCTCTCGCGGTAAAGCTCATACAGGAG 959
3
4 Oy 392 ATTAACAGGCTTACGCTGTAATGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 451
5 Db 870 ATTAACAGGCTTACGCTGTAATGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 959
6
7 Oy 452 GAAATCTCTCGGTAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 511
8 Db 990 GAAATCTCTCGGTAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1046

```

ADDRESSES: Henderson, Lind & Penick, I.L.P.
 1000 14th Street, N.W., #400
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20006

COMPUTER READABLE FORM:
 PRINTED ON 11x17 inch, 3.5 inch, 1.44 mb
 COMPUTER: IBM compatible

OPERATING SYSTEM: MS-DOS
 SOFTWARE: MicroDirect 5.1

CURRENT APPLICATION NUMBER: US/09/514,340
 APPLICATION NUMBER: 09/000,016

FILED DATE: 20-Feb-2000
 PUBLICATION DATE: 10-Mar-2001

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/000,016

RESISTANCE TO ANTIBIOTICS: 10, 945
 RESISTANCE TO ANTIBIOTICS: 10, 945

TELECOMMUNICATION INFORMATION: <UNKNOWN>
 TELEPHONE: 202-711-9200

TELEX: 90-000-0000
 FAX: 202-711-9200

TELETYPE: <UNKNOWN>
 TELETYPE: <UNKNOWN>

INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:

LENGTH: 2809 base pairs
 TYPE: nucleic acid

MOLECULE TYPE: genomic DNA
 ORIGINAL SOURCE: <UNKNOWN>

STRAIN: <UNKNOWN>
 FEATURE: <UNKNOWN>

NAME/KEY: CDS
 LOCATION: 338..2539

IDENTIFICATION METHOD: E
 NAME/KEY: CDS

LOCATION: 2540..2809
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-514-340-1
 Query Match

Best Local Similarity 54.3%; Score 191.6; Db 4; Length 2809;
 Matches 583; Conservative 0; Mismatches 439; Indels 46; Gaps 8;

332 GTATGACAGCAGCTTACTGCTGTACACAGAGGCTCGGAGATATCTACAGAGG 391

Db 970 GTGAGAGCAGCTTACTGCTGTACACAGAGGCTCGGAGATATCTACAGAGG 929

-Gy 392 ATACAGAGCTTACTGCTGTACACAGAGGCTCGGAGATATCTACAGAGG 451

Db 930 AGGAGAGCAGCTTACTGCTGTACACAGAGGCTCGGAGATATCTACAGAGG 989

Gy 432 GATACCTCTCTGCTGTACACAGAGGCTCGGAGATATCTACAGAGG 511

Db 990 GTGAGAGCAGCTTACTGCTGTACACAGAGGCTCGGAGATATCTACAGAGG 1046

Gy 512 AGGAGAGCAGCTTACTGCTGTACACAGAGGCTCGGAGATATCTACAGAGG 571

Db 1047 ATACAGAGCTTACTGCTGTACACAGAGGCTCGGAGATATCTACAGAGG 1103

Gy 572 GTGAGAGCAGCTTACTGCTGTACACAGAGGCTCGGAGATATCTACAGAGG 631

Db 1104 GTGAGAGCAGCTTACTGCTGTACACAGAGGCTCGGAGATATCTACAGAGG 1163

Gy 632 GTGAGAGCAGCTTACTGCTGTACACAGAGGCTCGGAGATATCTACAGAGG 688

512 AGGAGAGCAGCTTACTGCTGTACACAGAGGCTCGGAGATATCTACAGAGG 571

Db 1047 ATACAGAGCTTACTGCTGTACACAGAGGCTCGGAGATATCTACAGAGG 1103

Gy 572 GTGAGAGCAGCTTACTGCTGTACACAGAGGCTCGGAGATATCTACAGAGG 631

Db 1104 GTGAGAGCAGCTTACTGCTGTACACAGAGGCTCGGAGATATCTACAGAGG 1163

Gy 632 GTGAGAGCAGCTTACTGCTGTACACAGAGGCTCGGAGATATCTACAGAGG 688

Db 1164 GTGAGAGCAGCTTACTGCTGTACACAGAGGCTCGGAGATATCTACAGAGG 1223

Gy 748 GTGAGAGCAGCTTACTGCTGTACACAGAGGCTCGGAGATATCTACAGAGG 807

Db 1224 GTGAGAGCAGCTTACTGCTGTACACAGAGGCTCGGAGATATCTACAGAGG 1283

Gy 1284 GTGAGAGCAGCTTACTGCTGTACACAGAGGCTCGGAGATATCTACAGAGG 1343

Db 1343 GTGAGAGCAGCTTACTGCTGTACACAGAGGCTCGGAGATATCTACAGAGG 1402

Gy 1402 GTGAGAGCAGCTTACTGCTGTACACAGAGGCTCGGAGATATCTACAGAGG 1461

Db 1461 GTGAGAGCAGCTTACTGCTGTACACAGAGGCTCGGAGATATCTACAGAGG 1520

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Gy 1638 GTGAGAGCAGCTTACTGCTGTACACAGAGGCTCGGAGATATCTACAGAGG 1697

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RESULT 14

US-09-514-340-1

Publication US/0951340

Patent No. 6,619,897

GENERAL INFORMATION:

INVENTOR: ANANDA ET AL.

TITLE OF INVENTION: GENE ENCODING A PROTEIN HAVING ASHMTAC

HYDROLASE ACTIVITY FOR A SUBSTITUTED 1,4-DIHYDROXYKETONE

NUMBER OF SEQUENCES: 7

SEQUENCE INFORMATION:

SEQUENCE INFORMATION:

SEQUENCE INFORMATION:

SEQUENCE INFORMATION:

[illegible]

RESULT 15

118-00-000-016-1
CT 17053M

F-910-000-50-50

: sequence 3, Ag

Patent No. 614

: GENERAL INFORMATION

APPLICANT:

1 TITLE OF IN

10 TITLE OF INVENTION

IN 30 27111

NUMBER OF

CORRESPONDENCE:

ADDRESS

SUBJECT:

STREET: 3
CITY: 3

CITY: 117

STYLIS

COUNTRY:

CURRENT APPLICATION NUMBER: 027-9/1000-016
 CLASSIFICATION: 550 3C 1998
 PRIOR APPLICATION NUMBER: 027-9/1000-016
 FILING DATE: 1998-09-09
 ATTORNEY/AGENT INFORMATION:
 FIRM: 027-9/1000-016
 REGISTRATION NUMBER: 33 167
 REFERENCE/DOCID NUMBER: 027-9/1000-016
 TELEPHONE: 202-721-8230
 TELEFAX: 202-721-8230
 INFORMATION FOR SEQ ID NO: 1:
 SOURCE CHARACTERISTICS:
 ORGANISM: *Escherichia coli*
 STRAIN: NCTC 11637
 STANDARDS: NUCLEIC ACID
 TYPE: DOUBLE
 MOLECULE TYPE: genomic DNA
 ORIGINAL SOURCE: *Escherichia coli*
 STRAIN: A-316
 FEATURES:
 LOCATION: 338...2535
 INFORMATION TYPE: E

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Query Match

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[illegible]

Search completed: November 2, 2002, 11:26:38
Job time : 72.5 secs

GenScore version 5.1.3
Copyright (c) 1991 - 2002, Compugen Ltd.

On nucleic - nucleic search, using wv model

Run on: November 2, 2002, 10:33:33 : Search time 51.5 Seconds

12789/24 Million cell updates/sec
(4.6 minutes)

Title: US-09-841-553-2

Perfect score: 1977

Sequence: 1 ATGAGAGGTAGTGGCTGT.....AGGCGCTCTCTACGGG 1977

Scoring table: IDENTITY_WVC

Gapop 10.0, Gapext 1.0

Searched: 113279 seqs, 16457418 residues

Total number of hits satisfying chosen parameters: 620558

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*

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- 2: /csp2.6/prodata/2/pubseq/US97_PUBCONB.seq*
- 3: /csp2.6/prodata/2/pubseq/US97_PUBCONB.seq*
- 4: /csp2.6/prodata/2/pubseq/US97_PUBCONB.seq*
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- 12: /csp2.6/prodata/2/pubseq/US97_PUBCONB.seq*
- 13: /csp2.6/prodata/2/pubseq/US97_PUBCONB.seq*
- 14: /csp2.6/prodata/2/pubseq/US97_PUBCONB.seq*

Prod. No. is the number of results predicted by chance to have a
maximum match of the same length to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

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8	81.2	4.2	1320	10	US-09-841-553-2
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16	80.4	4.1	1320	10	US-09-841-553-2
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ALIGNMENTS

RESULT 1: US-09-841-553-2
Sequence 11: Application US/10090624
Patent No. US200201213541
APPLICANT: INFORMATION: HILTI
INVENTOR: INFORMATION: HILTI
APPLICANT: MORISHTA, M
INVENTOR: MORISHTA, M
APPLICANT: KATO, K
INVENTOR: KATO, K

TITLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERHOSTABLE
CURRENT APPLICATION NUMBER: US/10/090,624
CURRENT FILING DATE: 2003-07-06
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 11/669/1997
NUMBER OF SEQ TO NOS: 31
SOFTWARE: Patent in process
SEQ LENGTH: 1977

TYPE: DNA
FEATURE: Artificial Sequence
OTHER INFORMATION: Synthetic
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Best Local Similarity: 100.0%
Match Length: 1977, Conservative: 0, Minmatch: 0, Gaps: 0

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Best Local Similarity: 100.0%
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Query Match
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Seq ID NO: 11 is not Delated.


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RESULT 13
US-05-833-263-1058
Sequence 1058, Application US/09833263
Patent No US20050110347A1
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
APPLICANT: Nerg, Aijun
APPLICANT: Clapper, Jonathan B.
APPLICANT: Sokol, John A.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
TITLE OF INVENTION: DIAGNOSES OF COLON CANCER AND METHODS FOR THEIR USE
CURRENT APPLICANT 210121.47C1C2
CURRENT FILING DATE: 2001-04-10
NUMBER OF SEQ TD NOS: 1093
NUMBER OF SEQ TD NOS: 1093
SEQ ID NO 1058
SEQ ID NO 1058 for Windows version 3.0
LENGTH: 15720
TYPE: DNA
US-05-833-263-1058
US-05-833-263-1058

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D0 261 CCGGACATCATAGCTCTCTGTGCTTGGCGGCTTGAGCTGTGCTGGCGCTTCACGA 320
D0 1014 GGAAGGAGAGCTCAAGCGAGTGTGGCGCGCGGCTTGC -- ATCAAGCTGGCG 1070
D0 321 CCGCTGAGAACCGCGCGCTTGTCCAGTCTCTGCAGACTGTCTGAGACCGCG 380
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D0 381 CTGCGCGGAGCTTTCAGCGGATGCACTGCACTGGGAGTACCGGACGCTCGCGCT 440
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 Job time : 97.5 sec

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3: 526 GATCTGAAGGGCAGGTCTAGGTGTGACACCGCTTAAGAGCGGTCTACCGCCAC 885
 DB 1 GATCTGAAGGGCAGGTCTAGGTGTGACACCGCTTAAGAGCGGTCTACCGCCAC 885
 QY 566 GATCTGAAGGGCAGGTCTAGGTGTGACACCGCTTAAGAGCGGTCTACCGCCAC 885
 DB 61 GATCTGAAGGGCAGGTCTAGGTGTGACACCGCTTAAGAGCGGTCTACCGCCAC 885
 QY 646 TCCAGTGAAGAGGTCTAGGTGTGACACCGCTTAAGAGCGGTCTACCGCCAC 885
 DB 121 TCCAGTGAAGAGGTCTAGGTGTGACACCGCTTAAGAGCGGTCTACCGCCAC 885
 QY 708 GACGCTTGTGAGAGGTCTAGGTGTGACACCGCTTAAGAGCGGTCTACCGCCAC 885
 DB 768 GACGCTTGTGAGAGGTCTAGGTGTGACACCGCTTAAGAGCGGTCTACCGCCAC 885
 QY 766 GACGCTTGTGAGAGGTCTAGGTGTGACACCGCTTAAGAGCGGTCTACCGCCAC 885
 DB 241 GACGCTTGTGAGAGGTCTAGGTGTGACACCGCTTAAGAGCGGTCTACCGCCAC 885
 QY 816 GACGCTTGTGAGAGGTCTAGGTGTGACACCGCTTAAGAGCGGTCTACCGCCAC 885
 DB 301 GACGCTTGTGAGAGGTCTAGGTGTGACACCGCTTAAGAGCGGTCTACCGCCAC 885
 QY 886 GACGCTTGTGAGAGGTCTAGGTGTGACACCGCTTAAGAGCGGTCTACCGCCAC 885
 DB 361 GACGCTTGTGAGAGGTCTAGGTGTGACACCGCTTAAGAGCGGTCTACCGCCAC 885
 QY 946 GTCATACGCTGTGAGAGGTCTAGGTGTGACACCGCTTAAGAGCGGTCTACCGCCAC 885
 DB 421 GTCATACGCTGTGAGAGGTCTAGGTGTGACACCGCTTAAGAGCGGTCTACCGCCAC 885
 QY 1006 CGGACCGGAGAGGTCTAGGTGTGACACCGCTTAAGAGCGGTCTACCGCCAC 885
 DB 481 CGGACCGGAGAGGTCTAGGTGTGACACCGCTTAAGAGCGGTCTACCGCCAC 885
 QY 1066 CGGACCGGAGAGGTCTAGGTGTGACACCGCTTAAGAGCGGTCTACCGCCAC 885
 DB 541 CGGACCGGAGAGGTCTAGGTGTGACACCGCTTAAGAGCGGTCTACCGCCAC 885
 QY 1126 CGGACCGGAGAGGTCTAGGTGTGACACCGCTTAAGAGCGGTCTACCGCCAC 885
 DB 601 CGGACCGGAGAGGTCTAGGTGTGACACCGCTTAAGAGCGGTCTACCGCCAC 885
 QY 1186 CGGACCGGAGAGGTCTAGGTGTGACACCGCTTAAGAGCGGTCTACCGCCAC 885
 DB 661 CGGACCGGAGAGGTCTAGGTGTGACACCGCTTAAGAGCGGTCTACCGCCAC 885
 QY 1246 CGGACCGGAGAGGTCTAGGTGTGACACCGCTTAAGAGCGGTCTACCGCCAC 885
 DB 720 CGGACCGGAGAGGTCTAGGTGTGACACCGCTTAAGAGCGGTCTACCGCCAC 885
 QY 1306 CGGACCGGAGAGGTCTAGGTGTGACACCGCTTAAGAGCGGTCTACCGCCAC 885
 DB 780 CGGACCGGAGAGGTCTAGGTGTGACACCGCTTAAGAGCGGTCTACCGCCAC 885
 QY 1366 CGGACCGGAGAGGTCTAGGTGTGACACCGCTTAAGAGCGGTCTACCGCCAC 885
 DB 840 CGGACCGGAGAGGTCTAGGTGTGACACCGCTTAAGAGCGGTCTACCGCCAC 885
 QY 1426 G 1436
 DB 898 G 898
 RESULT 6
 ANT85679

ID ANT85679 standard; DMA; 568 BP.
 AC ANT85679;
 DT 20-APR-1998 (first ent.)
 XX Thermococcus protease fragment coding sequence.
 XX Thermococcus protease fragment coding sequence.
 XX Protease; research reagent; thermal stability; thermococcus oler; ss.
 XX Thermococcus oler DSM-3479.
 XX M09721823-AL.
 PN 19-JUN-1997.
 XX 07-NOV-1995; 95MO-JPO3173.
 XX 12-DEC-1995; 95ST-0323485.
 PA (TMI) TAKARA SHUJO CO. LTD.
 XX Abada K, Xiao J, Mito M, Morishita M, Takahara H.
 PT Tadamasa S, Tadamasa K.
 XX WPI: 1997-33279/30.
 CC This sequence represents a fragment of the coding sequence for the
 protease and gene encoding them obtained from Thermococcus oler
 (Proteococcus strains - have extremely high thermal stability and are
 useful industrially and as research reagents
 Disclosure: Page 114-115, 159pp; Japanese.
 CC This sequence represents a fragment of the coding sequence for the
 protease from Thermococcus oler DSM-2476 (extremely high thermal
 stability). This sequence encodes a fragment of the protease of the
 same organism. The protease has extremely high thermal
 stability. The protease can be used in the food, drug and chemical industries.
 CC Sequence 1454 BP: 352 A; 352 C; 403 G; 357 T; 0 other.
 SQ Query Match 100%; Score 856.8; DB 18; Length 1454;
 Best Local Similarity 97.0%; Prod. No. 1.1e-14; Indels 0; Gaps 0;
 Matches 81; Conservative 0; Mismatches 7;

QY 1 ATGAGAGGTCTAGGTGTGACACCGCTTAAGAGCGGTCTACCGCCAC 60
 DB 61 ATGAGAGGTCTAGGTGTGACACCGCTTAAGAGCGGTCTACCGCCAC 60
 QY 647 GTCATACGCTGTGAGAGGTCTAGGTGTGACACCGCTTAAGAGCGGTCTACCGCCAC 706
 DB 647 GTCATACGCTGTGAGAGGTCTAGGTGTGACACCGCTTAAGAGCGGTCTACCGCCAC 706
 QY 707 GTCATACGCTGTGAGAGGTCTAGGTGTGACACCGCTTAAGAGCGGTCTACCGCCAC 766
 DB 707 GTCATACGCTGTGAGAGGTCTAGGTGTGACACCGCTTAAGAGCGGTCTACCGCCAC 766
 QY 121 GTCATACGCTGTGAGAGGTCTAGGTGTGACACCGCTTAAGAGCGGTCTACCGCCAC 766
 DB 767 GTCATACGCTGTGAGAGGTCTAGGTGTGACACCGCTTAAGAGCGGTCTACCGCCAC 766
 QY 181 GTCATACGCTGTGAGAGGTCTAGGTGTGACACCGCTTAAGAGCGGTCTACCGCCAC 826
 DB 767 GTCATACGCTGTGAGAGGTCTAGGTGTGACACCGCTTAAGAGCGGTCTACCGCCAC 826
 QY 241 GTCATACGCTGTGAGAGGTCTAGGTGTGACACCGCTTAAGAGCGGTCTACCGCCAC 900
 DB 887 GTCATACGCTGTGAGAGGTCTAGGTGTGACACCGCTTAAGAGCGGTCTACCGCCAC 900
 QY 301 GTCATACGCTGTGAGAGGTCTAGGTGTGACACCGCTTAAGAGCGGTCTACCGCCAC 946
 DB 947 GTCATACGCTGTGAGAGGTCTAGGTGTGACACCGCTTAAGAGCGGTCTACCGCCAC 1006
 QY 361 GTCATACGCTGTGAGAGGTCTAGGTGTGACACCGCTTAAGAGCGGTCTACCGCCAC 1066
 DB 1007 GTCATACGCTGTGAGAGGTCTAGGTGTGACACCGCTTAAGAGCGGTCTACCGCCAC 1066

QY	423	TGCTGCTCCAGATAGAGGCGGAGTACGTCGTGAACTCTCTGCTACGAGGAGCGT	1460
DB	1067	TGCTGCTCCAGATAGAGGCGGAGTACGTCGTGAACTCTCTGCTACGAGGAGCGT	1126
QY	481	GTGCTGCTCCAGATAGAGGCGGAGTACGTCGTGAACTCTCTGCTACGAGGAGCGT	510
DB	1127	GTGCTGCTCCAGATAGAGGCGGAGTACGTCGTGAACTCTCTGCTACGAGGAGCGT	1184
QY	541	GTGCTGCTCCAGATAGAGGCGGAGTACGTCGTGAACTCTCTGCTACGAGGAGCGT	600
DB	1187	GTGCTGCTCCAGATAGAGGCGGAGTACGTCGTGAACTCTCTGCTACGAGGAGCGT	1246
QY	601	GTGCTGCTCCAGATAGAGGCGGAGTACGTCGTGAACTCTCTGCTACGAGGAGCGT	660
DB	1247	GTGCTGCTCCAGATAGAGGCGGAGTACGTCGTGAACTCTCTGCTACGAGGAGCGT	1306
QY	661	GTGCTGCTCCAGATAGAGGCGGAGTACGTCGTGAACTCTCTGCTACGAGGAGCGT	720
DB	1307	GTGCTGCTCCAGATAGAGGCGGAGTACGTCGTGAACTCTCTGCTACGAGGAGCGT	1366
QY	721	GTGCTGCTCCAGATAGAGGCGGAGTACGTCGTGAACTCTCTGCTACGAGGAGCGT	780
DB	1367	GTGCTGCTCCAGATAGAGGCGGAGTACGTCGTGAACTCTCTGCTACGAGGAGCGT	1426
QY	781	AGGCTGCTCCAGATAGAGGCGGAGTACGTCGTGAACTCTCTGCTACGAGGAGCGT	818
DB	1427	AGGCTGCTCCAGATAGAGGCGGAGTACGTCGTGAACTCTCTGCTACGAGGAGCGT	1464

RESULT 7

AA185595

AA185595 standard; DNA, 1962 BP.

AC AA185595;

AC 20-APR-1998 (first entry)

XX Pyrococcus furiosus PFS protease coding sequence.

XX Protease; research reagent; thermal stability; pyrococcus furiosus; 38

XX Pyrococcus furiosus DSN-7618.

XX MOY71823-AL.

XX 15-JUN-1997.

XX 07-NOV-1996; 98NO-JP03133.

XX 12-DEC-1995; 95JP-032385.

XX (FAM) ; TAKARA SHUZO CO LTD.

XX Asada K, Kato J, Mitsu M, Morishita M, Takakura M.

XX Tsukuba S, Yamamoto S.

XX BP1: 1997-33274/20.

XX PFS; AMF4125.

XX Protease(s) and genes encoding them obtained from Pyrococcus

XX furiosus. The proteases have extremely high thermal

XX stability. The proteases can be used as research reagents, and

XX industrially in the food, drug and chemical industries.

XX

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cardiovascular; treatment: hypertension; ischemic heart disease. db

XX Streptomyces viridosporus.

XX Key Location/Qualifiers

XX 338..259

XX CDS

XX /note= "no stop codon given"

XX nise_feature

XX 950..2509

XX /note= "encodes AW13668"

XX W97070243-X1.

XX 13-FEB-1997.

XX 30-JUL-1995: 9480-JP02147.

XX 20-FEB-1994: 9450-0007478.

XX 31-JUL-1995: 9530-0212970.

XX (GNOC) MERICIAN CORP.

XX Arianse A, Dobashi K, Ishikawa T, Nakashima T;

XX Tsuruta T, Yoshio T;

XX WPI: 1997-145882/11.

XX P-9808; AW13668-01.

XX Asymmetric hydrolase gene derived from Streptomyces viridosporus -

XX acts on 4-substituted-1,4-di-hydroxyridine derivatives to produce

XX chiral derivatives useful for synthesis of cardiovascular drugs

XX Claim 3; Page 49-55; 78pp; Japanese.

XX This sequence is the Streptomyces viridosporus dhpA gene which encodes an

XX asymmetric hydrolase which acts on 4-substituted-1,4-dihydroxyridine

XX derivatives. The enzyme allows the efficient conversion of 4-substituted-

XX dihydroxyridine derivatives to 4-substituted-1,4-dihydroxyridine derivatives.

XX for use in the synthesis of cardiovascular drugs suitable for the

XX treatment of e.g. hypertension and ischemic heart disease.

XX Sequence 2539 bp; 433 A; 959 C; 867 G; 280 T; 0 other.

XX Query Match 9.7%; Score 130.5; DB 18; Length 2539;

XX Best Local Similarity 54.5%; Pos: 26-26;

XX Matches 58; Conservative 0; Nimaatches 639; Indels 48; Pape

XX 332 TGTACACAGCGTCTTCCTGCTACACAGAGGCTGCTGGGATCATACAGAGG 391

XX DO 870 TGTGGGAGCGCTCTCCACAGCGAGCGAGCGCTGCTGCTGCTGCTG 959

XX QY 392 ATTACAGAGTCTAGTTCACAGACCTCTTCCTGCTGCTGCTGCTGCTGCT 451

XX DO 930 TACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 989

XX QY 452 TACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 511

XX DO 990 DGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1046

XX QY 512 TACGAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 571

XX DO 1047 TACAGAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1103

XX QY 572 GGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 631

XX DO 1104 CGGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1163

XX QY 632 CGGCGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 688

XX DO 1164 CGGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1223

XX QY 689 TCAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 748

DB 1224 CGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1283

QY 749 GGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 809

DB 1284 GGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1331

QY 809 GGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 868

DB 1332 TGGAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1391

QY 869 GGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 929

DB 1392 GGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1445

QY 929 GGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 988

DB 1445 GGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1505

QY 989 GGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1045

DB 1506 GGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1565

QY 1046 GGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1100

DB 1566 GGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1625

QY 1101 GGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1156

DB 1625 GGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1685

QY 1157 GGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1216

DB 1686 GGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1745

QY 1217 GGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1276

DB 1746 GGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1796

QY 1277 GGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1336

DB 1797 GGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1856

QY 1337 GGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1386

DB 1857 TGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1906

XX RESULT 14

XX ANTS1455

XX ATG04455 standard; DNA; 2809 bp.

XX AC

XX AC

XX ATG04455;

XX DT

XX 06-OCT-1997 (first entry).

XX DhpA-mal chimeric gene.

XX KM asymmetric hydrolase; dhpA; 4-substituted-1,4-dihydroxyridine.

XX KM derivative; Streptomyces viridosporus; Streptomyces viridosporus.

XX KM Chimeric streptomyces viridosporus; Streptomyces viridosporus.

XX KM Chimeric streptomyces viridosporus; Streptomyces viridosporus.

XX KM Chimeric streptomyces viridosporus; Streptomyces viridosporus.

XX KM Chimeric streptomyces viridosporus; Streptomyces viridosporus.

XX KM Chimeric streptomyces viridosporus; Streptomyces viridosporus.

XX KM Chimeric streptomyces viridosporus; Streptomyces viridosporus.

XX KM Chimeric streptomyces viridosporus; Streptomyces viridosporus.

XX KM Chimeric streptomyces viridosporus; Streptomyces viridosporus.

XX KM Chimeric streptomyces viridosporus; Streptomyces viridosporus.

XX KM Chimeric streptomyces viridosporus; Streptomyces viridosporus.

XX KM Chimeric streptomyces viridosporus; Streptomyces viridosporus.

XX KM Chimeric streptomyces viridosporus; Streptomyces viridosporus.

XX KM Chimeric streptomyces viridosporus; Streptomyces viridosporus.

XX KM Chimeric streptomyces viridosporus; Streptomyces viridosporus.

XX KM Chimeric streptomyces viridosporus; Streptomyces viridosporus.

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XX KM Chimeric streptomyces viridosporus; Streptomyces viridosporus.

XX KM Chimeric streptomyces viridosporus; Streptomyces viridosporus.

XX KM Chimeric streptomyces viridosporus; Streptomyces viridosporus.

XX KM Chimeric streptomyces viridosporus; Streptomyces viridosporus.

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XX KM Chimeric streptomyces viridosporus; Streptomyces viridosporus.

XX KM Chimeric streptomyces viridosporus; Streptomyces viridosporus.

XX KM Chimeric streptomyces viridosporus; Streptomyces viridosporus.

XX KM Chimeric streptomyces viridosporus; Streptomyces viridosporus.

XX KM Chimeric streptomyces viridosporus; Streptomyces viridosporus.

Wed Nov 6 14:29:34 2002

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XX P-PSB; AB09483.
XX New DNA sequence of thermophilic protein decomposition enzyme and
XX protein derived therefrom.
XX
XX Claim 1; Page 6; 15pp: Korean.
XX
XX This sequence represents the DNA encoding the thermomaxibacter
XX yonsei subtilisin-like serine protease of the invention.
XX
XX Sequence 2121 BP; 712 A; 410 C; 425 G; 554 T; 20 other;
XX
XX Query Match: 97.1%; Score 386.6; Pos 23; Length 2121.
XX Similarity: 97.1%; Pos 23; Length 2121.
XX Mismatches 299; Indels 15; Gaps:
XX Matches 355; Conservative
XX
Oy 374 TAAAGTTCACACGAGGATACAGATGTCAGTTCAGTTCGACGCGACATTCGCTCCGGA 433
Db 374 TAAAGTTCACACGAGGATACAGATGTCAGTTCAGTTCGACGCGACATTCGCTCCGGA 433
Oy 434 TAGGGCGGATACGCTGCGACGCTCGCTGACGAGGAGCGCTGTGTGTGCCA 493
Db 434 TAGGGCGGATACGCTGCGACGCTCGCTGACGAGGAGCGCTGTGTGTGCCA 493
Oy 443 TGTGATCAGCAGACGAGGATGATTTGAGTACGAGGAGGATGATGATGATGAT 502
Db 443 TGTGATCAGCAGACGAGGATGATTTGAGTACGAGGAGGATGATGATGATGAT 502
Oy 494 TGTGATCAGCAGACGAGGATGATTTGAGTACGAGGAGGATGATGATGATGAT 550
Db 494 TGTGATCAGCAGACGAGGATGATTTGAGTACGAGGAGGATGATGATGATGAT 550
Oy 503 TTTATGACGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 562
Db 503 TTTATGACGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 562
Oy 551 GTTACGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 610
Db 551 GTTACGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 610
Oy 563 GGTAAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 622
Db 563 GGTAAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 622
Oy 611 TGTGATCAGCAGACGAGGATGATTTGAGTACGAGGAGGATGATGATGATGAT 670
Db 611 TGTGATCAGCAGACGAGGATGATTTGAGTACGAGGAGGATGATGATGATGAT 670
Oy 622 TGTGATCAGCAGACGAGGATGATTTGAGTACGAGGAGGATGATGATGATGAT 682
Db 622 TGTGATCAGCAGACGAGGATGATTTGAGTACGAGGAGGATGATGATGATGAT 682
Oy 683 ATGCTGTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 742
Db 683 ATGCTGTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 742
Oy 731 TGTGATCAGCAGACGAGGATGATTTGAGTACGAGGAGGATGATGATGATGAT 790
Db 731 TGTGATCAGCAGACGAGGATGATTTGAGTACGAGGAGGATGATGATGATGAT 790
Oy 743 TACTGCGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 802
Db 743 TACTGCGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 802
Oy 850 ACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 850
Db 850 ACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 850
Oy 851 ACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 851
Db 851 ACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 851
Oy 863 ATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 921
Db 863 ATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 921
Oy 911 CTATACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 935
Db 911 CTATACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 935
Oy 923 ATATACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 943
Db 923 ATATACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 943
Oy 959 GTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1018
Db 959 GTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1018
Oy 983 ATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1042
Db 983 ATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1042
Oy 1019 GAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1067
Db 1019 GAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1067
Oy 1043 GAGATTAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1091
Db 1043 GAGATTAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1091

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Search completed: November 2, 2002, 08:28:13
 Job time : 303 sec

PS Claim 9, Page 92-95, 199pp. Japanese.

CC This sequence is a process of the invention. The process of the
CC invention have extremely high thermal stability. The process of the
CC invention are used as a research reagent, and industrially in the food, drug and
CC chemical industries.

XX Sequence 655 AA;

Query Match 100.0%; Score 3428; DB 18; Length 655;

Best Local Similarity 88.18; Pct. Ident. 100.0%; Indels 0; Gaps 0;

Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGGLALLIVLVLGVGVAAAPPEKVKYVNNVYVNTGLLPTKQLNMRIS 60

Db 1 MGGLALLIVLVLGVGVAAAPPEKVKYVNNVYVNTGLLPTKQLNMRIS 60

Qy 61 TTVVFNHREKAEIAVVELEHQAQVYVTHITPAADLVKLVLLVSLGDAKLSGV 120

Db 61 TTVVFNHREKAEIAVVELEHQAQVYVTHITPAADLVKLVLLVSLGDAKLSGV 120

Qy 121 RTFQEDKVTYVALELDQESAAQVNTYVHGLTDSGTTIGDGDASHEDLQGV 180

Db 121 RTFQEDKVTYVALELDQESAAQVNTYVHGLTDSGTTIGDGDASHEDLQGV 180

Qy 122 RTFQEDKVTYVALELDQESAAQVNTYVHGLTDSGTTIGDGDASHEDLQGV 180

Db 122 RTFQEDKVTYVALELDQESAAQVNTYVHGLTDSGTTIGDGDASHEDLQGV 180

Qy 181 IGWVFNHREKAEIAVVELEHQAQVYVTHITPAADLVKLVLLVSLGDAKLSGV 240

Db 181 IGWVFNHREKAEIAVVELEHQAQVYVTHITPAADLVKLVLLVSLGDAKLSGV 240

Qy 241 IETKAGVNNVYVNTGLLPTKQLNMRIS 300

Db 241 IETKAGVNNVYVNTGLLPTKQLNMRIS 300

Qy 301 GPMVTVGSPAANKVTVGADVDNINASTSPFTAGELFEVAVQVGLAPAG 360

Db 301 GPMVTVGSPAANKVTVGADVDNINASTSPFTAGELFEVAVQVGLAPAG 360

Qy 361 TSNPTFINDVTSKTSMTAPHSVGVALLQAPSPDFQVTKALLETATAPKEIA 420

Db 361 TSNPTFINDVTSKTSMTAPHSVGVALLQAPSPDFQVTKALLETATAPKEIA 420

Qy 421 DIATGAGVNNVYVNTGLLPTKQLNMRIS 480

Db 421 DIATGAGVNNVYVNTGLLPTKQLNMRIS 480

Qy 481 DLVYIDPNVDVNTATGTFEGVGVNFTAGVTVVYVSKGAMQVGVDSGLQ 540

Db 481 DLVYIDPNVDVNTATGTFEGVGVNFTAGVTVVYVSKGAMQVGVDSGLQ 540

Qy 541 SGQGNHNPENPPTVDTQVTVGVNTVDSCTFVNNVSKATIGLTFSTND 600

Db 541 SGQGNHNPENPPTVDTQVTVGVNTVDSCTFVNNVSKATIGLTFSTND 600

Qy 601 LDLLYDPMNGLVDRSTSENSTENAPGCTVFLTATSTGNATQALVITG 659

Db 601 LDLLYDPMNGLVDRSTSENSTENAPGCTVFLTATSTGNATQALVITG 659

RESULT 2

AMW4129

ID AMW4129 standard; Protein: 654 AA.

AC AMW4129

AC AMW4129

XX 20-APR-1998 (first entry)

XX Proteococcus furiosus protease PRUS.

DE Proteococcus furiosus protease PRUS.

XX Protease; research reagent; thermal stability; pyrococcus furiosus

XX Proteococcus furiosus DSM-3638.

XX W09721823-A1.

XX 19-JUN-1997.

PF 07-NOV-1996; 95NO-JP03253.

XX 12-DEC-1995; 95JP-032345.

PA (TAXI) TAKARA SHUJO CO LTD.

XX Asada K, Kato I, Mitsu M, Morishita M, Takabeura H.

XX 0875, 1997-31274/40.

PI Tamaoka S, Yamamoto K.

DB NPSB; PAT285655.

XX Protease and some analogs them obtained from thermococcus and

XX protease and some analogs them obtained from thermococcus and

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XX protease and some analogs them obtained from thermococcus and

XX protease and some analogs them obtained from thermococcus and

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XX protease and some analogs them obtained from thermococcus and

XX protease and some analogs them obtained from thermococcus and

CC (optimum 6-9), and retains more than 50% of its activity after 8 hours at 55 deg C. The invention also provides a method for producing a polypeptide of formula SIG-Ala-gly-gly-an-PHO, where SIG is a signal peptide from subtilisin, and PHO is the above protease. Host cells are used for the recombinant production of the protease. The genes are used for the recombinant production of the protease. The hyperthermostable protease which can be prepared in quantity suitable for industrial use, can be used as an additive for drugs, washing agents, and foodstuffs and for chemical synthesis.

XX Sequence 522 AA:

Query Match 68.5%; Score 3149.5; DB 20; Length 522;
Best Local Similarity 82.2%; Pred. No. 4.5e-141; Indels 5; Gaps 1;
Matches 449; Conservative 42; Mismatches 31

QY 133 ALEGLSDAQAQVYVWNGDSTIGTIGTIDGASHPDQGVGVWVNGEST 192
DB 1 ALEGLSDAQAQVYVWNGDSTIGTIGTIDGASHPDQGVGVWVNGEST 60
QY 193 PFDHGGTGVASVAMTGAQKSTGMAQKAGVAGDGGSGSTITIGVNAV 352
DB 61 PFDHGGTGVASVAMTGAQKSTGMAQKAGVAGDGGSGSTITIGVNAV 120
QY 253 DNDKQGTGVASVAMTGAQKSTGMAQKAGVAGDGGSGSTITIGVNAV 120
DB 121 DNDKQGTGVASVAMTGAQKSTGMAQKAGVAGDGGSGSTITIGVNAV 180
QY 313 ASVITGVAVDSVMDIAESGSGSDGTALGQVAVAGDGGSGSTITIGVNAV 180
DB 313 ASVITGVAVDSVMDIAESGSGSDGTALGQVAVAGDGGSGSTITIGVNAV 240
QY 373 ASGTSTNATFVSQVGLTQAFSPMTDKVKTALSTADVAPAEIATAGGVNAV 432
DB 241 ASGTSTNATFVSQVGLTQAFSPMTDKVKTALSTADVAPAEIATAGGVNAV 300
QY 433 KAIKDTQALYALFTFSGVAVGSGSTITIGTIDGASHPDQGVGVWVNGEST 492
DB 301 KAIKDTQALYALFTFSGVAVGSGSTITIGTIDGASHPDQGVGVWVNGEST 360
QY 493 DYSTATGVKGVKVFAGTGVAVYVSGANTGVVDSGLSGGGGVWVNGEST 552
DB 361 DYSTATGVKGVKVFAGTGVAVYVSGANTGVVDSGLSGGGGVWVNGEST 420
QY 553 PFTPTVDTQGVNDVHDSPTGVWVNGSGTITIGTIDGASHPDQGVGVWVNGEST 612
DB 416 PFTPTVDTQGVNDVHDSPTGVWVNGSGTITIGTIDGASHPDQGVGVWVNGEST 475
QY 633 VDSGTSSVSEVETAPVAFVFWVNSSTGADQALQAVYVG 659
DB 476 VDSGTSSVSEVETAPVAFVFWVNSSTGADQALQAVYVG 522

RESULT 8
AMH4836
ID AMH4836 standard; protein; 412 AA.

XX AC AMH4836:

XX 06-MAY-1999 (first entry)

XX Hyperthermostable protease fragment.

XX additive; drug; washing agent; foodstuff; chemical synthesis.

XX Pyrococcus furiosus.

XX W0956626-A1.

XX 17-OCT-1998.

XX 04-JUN-1998: 99NO-J020465.

XX 10-JUN-1997: 97NP-0151949.
XX (AA1) TAKARA SHUZO CO LTD.
XX TAKARA K, Kato I, Morishita M, Shimojo T, Takakura H.
XX US1: 1999-080907/07.
XX M-PSDB: AM05520.

Recombinant hyperthermostable protease from *Pyrococcus furiosus* - for industrial use, for large scale production of the protease for industrial use.

XX Claim 2: Page 33-37; Paper: Japanese.

CC The invention relates to a hyperthermostable protease derived from a *Pyrococcus furiosus* (strain 122-27) (ATCC 49069). The protease has a working temperature of 110 deg C (optimum 80-95 deg C), and retains more than 50% of its activity after 8 hours at 55 deg C. The invention also provides gene sequences encoding a polypeptide of formula SIG-Ala-gly-gly-an-PHO, where SIG is a signal peptide from subtilisin, and PHO is the above protease. Host cells (especially *Escherichia coli* strains) transformed with vectors comprising the hyperthermostable protease gene can be used for the recombinant production of the hyperthermostable protease which can be prepared in quantity suitable for industrial use, can be used as an additive for drugs, washing agents, and foodstuffs and for chemical synthesis.

XX Sequence 412 AA:

Query Match 56.0%; Score 1018; DB 20; Length 412;
Best Local Similarity 89.5%; Pred. No. 7.8e-114;
Matches 367; Conservative 15; Mismatches 28; Indels 0; Gaps 0;

QY 133 ALEGLSDAQAQVYVWNGDSTIGTIGTIDGASHPDQGVGVWVNGEST 192
DB 1 ALEGLSDAQAQVYVWNGDSTIGTIGTIDGASHPDQGVGVWVNGEST 60
QY 193 PFDHGGTGVASVAMTGAQKSTGMAQKAGVAGDGGSGSTITIGVNAV 252
DB 61 PFDHGGTGVASVAMTGAQKSTGMAQKAGVAGDGGSGSTITIGVNAV 120
QY 253 DNDKQGTGVASVAMTGAQKSTGMAQKAGVAGDGGSGSTITIGVNAV 120
DB 121 DNDKQGTGVASVAMTGAQKSTGMAQKAGVAGDGGSGSTITIGVNAV 180
QY 313 ASVITGVAVDSVMDIAESGSGSDGTALGQVAVAGDGGSGSTITIGVNAV 180
DB 313 ASVITGVAVDSVMDIAESGSGSDGTALGQVAVAGDGGSGSTITIGVNAV 240
QY 373 ASGTSTNATFVSQVGLTQAFSPMTDKVKTALSTADVAPAEIATAGGVNAV 432
DB 241 ASGTSTNATFVSQVGLTQAFSPMTDKVKTALSTADVAPAEIATAGGVNAV 300
QY 433 KAIKDTQALYALFTFSGVAVGSGSTITIGTIDGASHPDQGVGVWVNGEST 492
DB 301 KAIKDTQALYALFTFSGVAVGSGSTITIGTIDGASHPDQGVGVWVNGEST 360
QY 493 DYSTATGVKGVKVFAGTGVAVYVSGANTGVVDSGLSGGGGVWVNGEST 552
DB 361 DYSTATGVKGVKVFAGTGVAVYVSGANTGVVDSGLSGGGGVWVNGEST 420

RESULT 9

AMH87005

XX AMH87005 standard; Protein; 237 AA.

XX AC AMH87005:

XX 10-MAY-1996 (first entry)

XX Hyperthermostable protease.

05-09-445-472-16
 Query Match 87.4% Score 2997.5; DB 4; Length 654;
 Best Local Similarity 83.2% Pct No. 3a-304
 Matches 562; Conservative 22; Mismatches 20; Indels 5; Gaps 1;
 05-09-445-472-16
 Patent No. 6355726
 GENERAL INFORMATION: HIRAKU
 APPLICANT: MORISGITA, MIO
 APPLICANT: SHINOBU, TOSHIKO
 APPLICANT: MITSU, MASAHITO
 APPLICANT: KATO, JUNSHIN
 TITLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERHYPERSTABLE
 CURRENT APPLICANT: TANAKURA
 CURRENT FILING DATE: 1999-12-05
 PRIOR APPLICATION NUMBER: 151969/1997
 NUMBER OF SEQ ID NOS: 3
 SOFTWARE: PatentIn version 3.0
 SIZE OF SEQ ID NOS: 33
 LENGTH: 654
 TYPE: PRT
 METHOD: PROCOCOC FURTOSU
 US-09-445-472-16

05-09-445-472-16
 Query Match 87.4% Score 2997.5; DB 4; Length 654;
 Best Local Similarity 83.2% Pct No. 3a-304
 Matches 562; Conservative 22; Mismatches 20; Indels 5; Gaps 1;
 05-09-445-472-16
 Patent No. 6355726
 GENERAL INFORMATION: HIRAKU
 APPLICANT: MORISGITA, MIO
 APPLICANT: SHINOBU, TOSHIKO
 APPLICANT: MITSU, MASAHITO
 APPLICANT: KATO, JUNSHIN
 TITLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERHYPERSTABLE
 CURRENT APPLICANT: TANAKURA
 CURRENT FILING DATE: 1999-12-05
 PRIOR APPLICATION NUMBER: 151969/1997
 NUMBER OF SEQ ID NOS: 3
 SOFTWARE: PatentIn version 3.0
 SIZE OF SEQ ID NOS: 33
 LENGTH: 654
 TYPE: PRT
 METHOD: PROCOCOC FURTOSU
 US-09-445-472-16

05-09-834-818-1
 Query Match 85.0% Score 3014; DB 4; Length 659;
 Best Local Similarity 83.2% Pct No. 3a-304
 Matches 562; Conservative 16; Mismatches 16; Indels 16; Gaps 7;
 05-09-834-818-1
 Sequence 1, Application US/088948188
 GENERAL INFORMATION:
 APPLICANT: TANAKURA, HIRAKU
 APPLICANT: MORISGITA, MIO
 APPLICANT: SHINOBU, TOSHIKO
 APPLICANT: MITSU, MASAHITO
 APPLICANT: KATO, JUNSHIN
 TITLE OF INVENTION: HYPERHYPERSTABLE PROTEASE GENES
 CURRENT APPLICANT: TANAKURA
 CURRENT FILING DATE: 1999-12-05
 PRIOR APPLICATION NUMBER: 151969/1997
 NUMBER OF SEQ ID NOS: 3
 SOFTWARE: PatentIn version 3.0
 SIZE OF SEQ ID NOS: 33
 LENGTH: 654
 TYPE: PRT
 METHOD: PROCOCOC FURTOSU
 US-09-834-818-1

05-09-834-818-1
 Query Match 85.0% Score 3014; DB 4; Length 659;
 Best Local Similarity 83.2% Pct No. 3a-304
 Matches 562; Conservative 16; Mismatches 16; Indels 16; Gaps 7;
 05-09-834-818-1
 Sequence 1, Application US/088948188
 GENERAL INFORMATION:
 APPLICANT: TANAKURA, HIRAKU
 APPLICANT: MORISGITA, MIO
 APPLICANT: SHINOBU, TOSHIKO
 APPLICANT: MITSU, MASAHITO
 APPLICANT: KATO, JUNSHIN
 TITLE OF INVENTION: HYPERHYPERSTABLE PROTEASE GENES
 CURRENT APPLICANT: TANAKURA
 CURRENT FILING DATE: 1999-12-05
 PRIOR APPLICATION NUMBER: 151969/1997
 NUMBER OF SEQ ID NOS: 3
 SOFTWARE: PatentIn version 3.0
 SIZE OF SEQ ID NOS: 33
 LENGTH: 654
 TYPE: PRT
 METHOD: PROCOCOC FURTOSU
 US-09-834-818-1

APPLICATION NUMBER:

ATTENDING CENTER INFORMATION:

NAME: Warren N. Choo, Jr.

REGISTRATION NUMBER: 33-367

TELEPHONE: 202-721-8200

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-721-8200

TELEFAX: 202-721-8230

TELEX:

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 734 amino acids

TYPE: amino acid

STRANDEDNESS: single

MOLECULE TYPE: Protein

US-09-000-016-4

Query Match 20.24; Score 692.5; 08 4; Length 734;
 Best Local Similarity 33.64; Fred. No. 26-42;
 Matches 202; Conservative 62; Mismatches 223; Indels 113; Gaps 21.

Qy 110 LTQGLKALSGVRFIDENYKVTVAELGELGSAQVWATYWNKLGDSGITIGITOTI 169
 Db 182 VTGROPTASIGAMPLD-----GVRRALGSLGSGVGGAPKASNGTGDGVYIAVLDTGV 236
 Qy 170 DASHPOUGKVIQWOTYHPTFDTHGHTHVAATAGTGAAGKATGNKAPKAG 229
 Db 237 DTSPDLGKGVNTAMPK-ACDVGKGTHTVASTAGTGAASKKTVGVAGAILN 295
 Qy 230 KNGVAGSGSISTITLOVSHVEMKDTGLKVTNLSGSGSSGSDTSLGAVNAN 288
 Db 286 GNVLDGSGEDGSLAGNEMA-----AGAAVTNLSGNDTSE-TPDEAVNLSAE 350
 Qy 289 AGTVGVAGSGSPNTWTCGSPAASKVITGVNGSNDLSGFSERP-TPDGLAPDEV 327
 Db 351 KQYLAIAANGDPE--STGSPGADALTVGADKKLAUTSTGPDGLAIPDVT 408
 Qy 348 ARGVOTIAPASSTGNCPIND---YTTNASTGSMATPHYSVGVALLQANPSITPKV 404
 Db 409 ARGVOTIAPASNGNDIGDGPAGTITSGTSMATPHYAGAILQKQHPMTSAELK 468
 Qy 405 TALEITADIVAREADIVAGAGVNYVYAK-----GVRRALGSLGSGVGGAPKASNGTGDGVYIAVLDTGV 236
 Db 469 GAI--TGSTGK--YTFPESGSLGNDLQAGVLDVAPSVSGVQVHPDDEVTQ 525
 Qy 437 -----TDVALKUTTGKSVUNGKSAFTDVGATFTYTLNLDGSDIDLYLIDPM 488
 Db 526 LTRNMGTDVTLTSTATDKGAKPAFTGLTATVTVVA---GGASVNDTAUTEL 582
 Qy 489 GIKRKYSTAVTGVKGVYVTPAGTNYVYKST-----KCAATGVQVDDVDS 537
 Qy 583 GGVYKATSVAYVGGGVYATVAARVERSTDVYHKGROGPTTELLDTAG 642
 Qy 536 LSGSGGGRPHNPHTPTDQTF-----TGS-VNDVDPGSDITM-----HNKSA 585
 Db 643 LSGSDCTG-----APATQATDILKALPTLVSHNDAFDPTAGIDMLVQPLSV 693
 Qy 586 TLTIQDITFDV-SYMLDVLDTLMDNDGTSISTENKFNKAPKATWTFVATST 644
 Db 694 TGT-TLLTLLMTTAMTADIVPK-----MPELAT-----TGTITOT 731
 Qy 645 TG 646
 Db 732 AG 733

RESULT 11

US-09-000-016-2

Sequence 2; Application US/0900016

GENERAL INFORMATION:

APPLICANT: ALIO ARISANA ET AL.
 TITLE OF INVENTION: GENE ENCODING A PROTEIN HAVING ASYMMETRIC
 REGISTRATION NUMBER: 33-367
 NUMBER OF SEQUENCES: 7
 COMPLETION DATE: 1998
 ADDRESS: National Institutes of Health
 ADDRESS: Bethesda, MD 20892
 STREET: 303 K Street, N.W., 1800
 STATE: Washington
 COUNTRY: U.S.A.

ZIP: 20005
 CHARGES: \$1000.00
 MEDIUM TYPE: Diskette, 3.5 Inch, 1.44 mb
 COMPUTER: IBM compatible
 SOFTWARE: GENSTAT, GENSTAT
 SOFTWARE: Mordant, 5.1
 CURRENT APPLICATION DATA: 9/100.016
 FILING DATE: 1998
 FILING DATE: 1998
 CLASSIFICATION: 530
 PRIOR APPLICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: NATIONAL INSTITUTES OF HEALTH
 REGISTRATION NUMBER: 33-367
 REFERENCE/DOCKET NUMBER:
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-721-8200
 TELEFAX: 202-721-8230
 TELEX:
 INVENTION FOR SEQ ID NO: 2:
 LENGTH: 823 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 MOLECULE TYPE: Protein
 US-09-000-016-2

Query Match Similarity 10.24; Score 692.5; Db 4; Length 823;
 Matches 202; Conservative 62; Mismatches 223; Indels 115; Gaps 21.

Qy 110 LTQGLKALSGVRFIDENYKVTVAELGELGSAQVWATYWNKLGDSGITIGITOTI 169
 Db 182 VTGROPTASIGAMPLD-----GVRRALGSLGSGVGGAPKASNGTGDGVYIAVLDTGV 236
 Qy 170 DASHPOUGKVIQWOTYHPTFDTHGHTHVAATAGTGAAGKATGNKAPKAG 229
 Db 237 DTSPDLGKGVNTAMPK-ACDVGKGTHTVASTAGTGAASKKTVGVAGAILN 295
 Qy 230 KNGVAGSGSISTITLOVSHVEMKDTGLKVTNLSGSGSSGSDTSLGAVNAN 288
 Db 286 GNVLDGSGEDGSLAGNEMA-----AGAAVTNLSGNDTSE-TPDEAVNLSAE 350
 Qy 289 AGTVGVAGSGSPNTWTCGSPAASKVITGVNGSNDLSGFSERP-TPDGLAPDEV 327
 Db 351 KQYLAIAANGDPE--STGSPGADALTVGADKKLAUTSTGPDGLAIPDVT 408
 Qy 348 ARGVOTIAPASSTGNCPIND---YTTNASTGSMATPHYSVGVALLQANPSITPKV 404
 Db 409 ARGVOTIAPASNGNDIGDGPAGTITSGTSMATPHYAGAILQKQHPMTSAELK 468
 Qy 405 TALEITADIVAREADIVAGAGVNYVYAK-----GVRRALGSLGSGVGGAPKASNGTGDGVYIAVLDTGV 236
 Db 469 GAI--TGSTGK--YTFPESGSLGNDLQAGVLDVAPSVSGVQVHPDDEVTQ 525
 Qy 437 -----TDVALKUTTGKSVUNGKSAFTDVGATFTYTLNLDGSDIDLYLIDPM 488
 Db 526 LTRNMGTDVTLTSTATDKGAKPAFTGLTATVTVVA---GGASVNDTAUTEL 582

ORIGINAL SOURCE:
ORGANISM: Bacillus
Strain: Carlsberg
US-07-72-087-4

Query Match 15.24 Score 554.5, E0.31, Length 378;
Similarity 34.24, Prod No. 8.7e+33;
Matches 149: Conservative 64; Mismatches 150; Indels 73; Gaps 13;
3 GLEALIVLVGLVGVSAAPKAEVDEYVYKGLLTPLFRILQKLNKELVW 63
DB 10 GMLTALFTMTASASAAQAK -----NVEQI
QY 63 IVERNREKIAIVLELGAARVYVTHITAIAGLAVREGLVLSIGTGKALSGTF 122
DB 42 VGHSSOKTASYNDIESGKVGKGRFIRIRANAKLDELKVK-----NDPUNV 94
QY 123 IQEYKVTYSLEGLDESAUVATYNNIGTDSGITIGDGLASHPLQGRYTG 182
DB 95 VEER:--VANALQVTPPGIPLKADKYAAGFGKAWKAVVLTGICASEPL--NYVL 150
QY 183 WCYNMRSPYDDHGGHNVASTAMTQASMK--TKGNQANALAKIKVLQAGSG 240
DB 151 GASTYAGENVTDGNGHFW----ACTVAALNTGTGLVAVSVLAVKVLNSGSGT 206
QY 241 IETIKVGVNVDREKKTGTITNIGLSSQSGTGLSELQANNNAPQNTVVCVAGNS 300
DB 207 YGIVSGIEMATN---GNQVIMELG---GGGSTMQRQVNDATARQVYVYAMONS 259
QY 303 GP--MTTGTGPAARVTVYVANGDNQNLASFSSGKPTADGLAPETVAPQDIAPR 358
DB 260 GSSGNTMTGTGPAKTDVAVGVDSINRHSFSSVG-----ALELWFGQGTSTP 313
QY 356 SGTSMCTPINDYTAASGTSMATPDSGVGALLQAHPSFKPKVKTALLETADVAPPE 418
DB 314 TST-----TATLMTGSPENQANALILSRHPLSASQVNRNLSSTNTLG--- 361
QY 419 IADTAGGRVNTYA 434
DB 352 SSFYTGGLINLEAK 376

Search completed: October 31, 2002, 13:31:28
Job time : 15 secs